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SEQUENCE LISTING

<110> Dr. Völkel, Helge

<120> Method for screening of modulators of calcineurin activity

<130> A34157PCT

<140> PCT/EP99/05220

<141> 1999-07-22

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<170> PatentIn Ver. 2.1

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Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu

SUBSTITUTE SHEET (RULE 26)

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 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
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 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
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 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
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 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
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 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
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 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
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Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
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Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
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Lys Glu Gly Arg Val Asp Glu Glu Ile Ala Leu Arg Ile Ile Asn Glu
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Gly Ala Ala Ile Leu Arg Arg Glu Lys Thr Met Ile Glu Val Glu Ala
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Tyr Leu Trp Val Leu Lys Ile Leu Tyr Pro Ser Thr Leu Phe Leu Leu
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Arg Gly Asn His Glu Cys Arg His Leu Thr Glu Tyr Phe Thr Phe Lys
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Gln Glu Cys Lys Ile Lys Tyr Ser Glu Arg Val Tyr Glu Ala Cys Met
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Glu Ala Phe Asp Ser Leu Pro Leu Ala Ala Leu Leu Asn Gln Gln Phe
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Leu Cys Val His Gly Gly Leu Ser Pro Glu Ile His Thr Leu Asp Asp
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Ile Arg Arg Leu Asp Arg Phe Lys Glu Pro Pro Ala Phe Gly Pro Met

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Ser Gln Glu His Phe Ser His Asn Thr Val Arg Gly Cys Ser Tyr Phe						
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Tyr Asn Tyr Pro Ala Val Cys Glu Phe Leu Gln Asn Asn Asn Leu Leu						
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Ser Ile Ile Arg Ala His Glu Ala Gln Asp Ala Gly Tyr Arg Met Tyr						
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Arg Lys Ser Gln Thr Thr Gly Phe Pro Ser Leu Ile Thr Ile Phe Ser						
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Ala Pro Asn Tyr Leu Asp Val Tyr Asn Asn Lys Ala Ala Val Leu Lys						
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Tyr Glu Asn Asn Val Met Asn Ile Arg Gln Phe Asn Cys Ser Pro His						
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Pro Tyr Trp Leu Pro Asn Phe Met Asp Val Phe Thr Trp Ser Leu Pro						
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Phe Val Gly Glu Lys Val Thr Glu Met Leu Val Asn Val Leu Ser Ile						
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Cys Ser Asp Asp Glu Leu Met Thr Glu Gly Glu Asp Gln Phe Asp Gly						
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Gly Lys Met Ala Arg Val Phe Ser Val Leu Arg Glu Glu Ser Glu Ser						
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Val Leu Thr Leu Lys Gly Leu Thr Pro Thr Gly Met Leu Pro Ser Gly						
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Val Leu Ala Gly Gly Arg Gln Thr Leu Gln Ser Ala Thr Val Glu Ala						
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Ile Glu Ala Glu Lys Ala Ile Arg Gly Phe Ser Pro Pro His Arg Ile						
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Cys Ser Phe Glu Glu Ala Lys Gly Leu Asp Arg Ile Asn Glu Arg Met						
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Pro Pro Arg Lys Asp Ala Val Gln Gln Asp Gly Phe Asn Ser Leu Asn						
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 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
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 Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser
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 Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
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 Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
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Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys				
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ctg gag tac aac tac aac agc cac aac gtc tat atc atg gcc gac aag				1083
Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys				
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Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu				
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Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile				
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Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln				
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tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg				1275
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu				
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Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu				
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Tyr Lys Ser Gly Leu Arg Ser Arg Ser Met Ser Gly Arg Arg Phe His				
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Leu Ser Thr Thr Asp Arg Val Ile Lys Ala Val Pro Phe Pro Pro Thr				
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Gln Arg Leu Thr Phe Lys Glu Val Phe Glu Asn Gly Lys Pro Lys Val				
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gat gtt tta aaa aac cat ttg gta aag gaa gga cga ctg gaa gag gaa				1515
Asp Val Leu Lys Asn His Leu Val Lys Glu Gly Arg Leu Glu Glu Glu				
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gta gcc tta aag ata atc aat gat ggg gct gcc atc ctg agg caa gag				1563
Val Ala Leu Lys Ile Ile Asn Asp Gly Ala Ala Ile Leu Arg Gln Glu				
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aag act atg ata gaa gta gat gct cca atc aca gta tgt ggt gat att				1611
Lys Thr Met Ile Glu Val Asp Ala Pro Ile Thr Val Cys Gly Asp Ile				
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cat gga caa ttc ttt gac cta atg aag tta ttt gaa gtt gga gga tca				1659
His Gly Gln Phe Phe Asp Leu Met Lys Leu Phe Glu Val Gly Gly Ser				
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Pro Ser Asn Thr Arg Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg Gly				
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 His Pro Lys Thr Leu Phe Leu Leu Arg Gly Asn His Glu Cys Arg His
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gct gcc ctc tta aac cag cag ttt ctc tgt gta cat gga gga atg tca 1947
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 <213> Homo sapiens

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 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser

165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
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 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 225 230 235

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 50 55 60
 Leu Lys Ile Ile Asn Asp Gly Ala Ala Ile Leu Arg Gln Glu Lys Thr
 65 70 75 80
 Met Ile Glu Val Asp Ala Pro Ile Thr Val Cys Gly Asp Ile His Gly
 85 90 95
 Gln Phe Phe Asp Leu Met Lys Leu Phe Glu Val Gly Gly Ser Pro Ser
 100 105 110
 Asn Thr Arg Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg Gly Tyr Phe
 115 120 125
 Ser Ile Glu Cys Val Leu Tyr Leu Trp Ser Leu Lys Ile Asn His Pro
 130 135 140
 Lys Thr Leu Phe Leu Leu Arg Gly Asn His Glu Cys Arg His Leu Thr
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 Asp Tyr Phe Thr Phe Lys Gln Glu Cys Arg Ile Lys Tyr Ser Glu Gln
 165 170 175
 Val Tyr Asp Ala Cys Met Glu Thr Phe Asp Cys Leu Pro Leu Ala Ala
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 Leu Leu Asn Gln Gln Phe Leu Cys Val His Gly Gly Met Ser Pro Glu
 195 200 205
 Ile Thr Ser Leu Asp Asp Ile Arg Lys Leu Asp Arg Phe Thr Glu Pro
 210 215 220

Pro Ala Phe Gly Pro Val Cys Asp Leu Leu Trp Ser Asp Pro Ser Glu
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 Asp Tyr Gly Asn Glu Lys Thr Leu Glu His Tyr Thr His Asn Thr Val
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 Arg Gly Cys Ser Tyr Phe Tyr Ser Tyr Pro Ala Val Cys Glu Phe Leu
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 Ala Gly Tyr Arg Met Tyr Arg Lys Ser Gln Ala Thr Gly Phe Pro Ser
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 385 390 395 400
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 Arg Gly Leu Asp Arg Ile Asn Glu Arg Met Pro Pro Arg Lys Asp Ser
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 <223> cathepsin-C cleavage site

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ggatcgcatt accatcacca tcacggatcc gcg acg aag gcc gtg tgc gtg ctg 174
                               Ala Thr Lys Ala Val Cys Val Leu
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Lys Gly Asp Gly Pro Val Gln Gly Ile Ile Asn Phe Glu Gln Lys Glu
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agt aat gga cca gtg aag gtg tgg gga agc att aaa gga ctg act gaa 270
Ser Asn Gly Pro Val Lys Val Trp Gly Ser Ile Lys Gly Leu Thr Glu
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ggc ctg cat gga ttc cat gtt cat gag ttt gga gat aat aca gca ggc 318
Gly Leu His Gly Phe His Val His Glu Phe Gly Asp Asn Thr Ala Gly
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tgt acc agt gca ggt cct cac ttt aat cct cta tcc aga aaa cac ggt 366
Cys Thr Ser Ala Gly Pro His Phe Asn Pro Leu Ser Arg Lys His Gly
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ggg cca aag gat gaa gag agg cat gtt gga gac ttg ggc aat gtg act 414
Gly Pro Lys Asp Glu Glu Arg His Val Gly Asp Leu Gly Asn Val Thr
 75                               80                               85

gct gac aaa gat ggt gtg gcc gat gtg tct att gaa gat tct gtg atc 462
Ala Asp Lys Asp Gly Val Ala Asp Val Ser Ile Glu Asp Ser Val Ile
 90                               95                               100

tca ctc tca gga gac cat tgc atc att ggc cgc aca ctg gtg gtc cat 510
Ser Leu Ser Gly Asp His Cys Ile Ile Gly Arg Thr Leu Val Val His
105                               110                               115                               120

gaa aaa gca gat gac ttg ggc aaa ggt gga aat gaa gaa agt aca aag 558
Glu Lys Ala Asp Asp Leu Gly Lys Gly Gly Asn Glu Glu Ser Thr Lys
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aca gga aac gct gga agt cgt ttg gct tgt ggt gta att ggg atc gcc 606
Thr Gly Asn Ala Gly Ser Arg Leu Ala Cys Gly Val Ile Gly Ile Ala
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3975

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 <213> Homo sapiens

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 35 40 45
 Glu Phe Gly Asp Asn Thr Ala Gly Cys Thr Ser Ala Gly Pro His Phe
 50 55 60
 Asn Pro Leu Ser Arg Lys His Gly Gly Pro Lys Asp Glu Glu Arg His
 65 70 75 80
 Val Gly Asp Leu Gly Asn Val Thr Ala Asp Lys Asp Gly Val Ala Asp
 85 90 95
 Val Ser Ile Glu Asp Ser Val Ile Ser Leu Ser Gly Asp His Cys Ile
 100 105 110
 Ile Gly Arg Thr Leu Val Val His Glu Lys Ala Asp Asp Leu Gly Lys
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 Gly Gly Asn Glu Glu Ser Thr Lys Thr Gly Asn Ala Gly Ser Arg Leu
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 Ala Cys Gly Val Ile Gly Ile Ala Gln
 145 150

 <210> 15
 <211> 3881
 <212> DNA
 <213> Homo sapiens

 <220>
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 <223> copper/zinc superoxide dismutase

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 <222> (577)..(582)
 <223> carboxypeptidase-A cleavage site

 <220>
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 <222> (578)..(603)
 <223> histidine tag

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 gcg acg aag gcc gtg tgc gtg ctg aag ggc gac ggc cca gtg cag ggc 165
 Ala Thr Lys Ala Val Cys Val Leu Lys Gly Asp Gly Pro Val Gln Gly
 5 10 15

 atc atc aat ttc gag cag aag gaa agt aat gga cca gtg aag gtg tgg 213
 Ile Ile Asn Phe Glu Gln Lys Glu Ser Asn Gly Pro Val Lys Val Trp
 20 25 30

gga agc att aaa gga ctg act gaa ggc ctg cat gga ttc cat gtt cat 261
 Gly Ser Ile Lys Gly Leu Thr Glu Gly Leu His Gly Phe His Val His
 35 40 45

gag ttt gga gat aat aca gca ggc tgt acc agt gca ggt cct cac ttt 309
 Glu Phe Gly Asp Asn Thr Ala Gly Cys Thr Ser Ala Gly Pro His Phe
 50 55 60 65

aat cct cta tcc aga aaa cac ggt ggg cca aag gat gaa gag agg cat 357
 Asn Pro Leu Ser Arg Lys His Gly Gly Pro Lys Asp Glu Glu Arg His
 70 75 80

gtt gga gac ttg ggc aat gtg act gct gac aaa gat ggt gtg gcc gat 405
 Val Gly Asp Leu Gly Asn Val Thr Ala Asp Lys Asp Gly Val Ala Asp
 85 90 95

gtg tct att gaa gat tct gtg atc tca ctc tca gga gac cat tgc atc 453
 Val Ser Ile Glu Asp Ser Val Ile Ser Leu Ser Gly Asp His Cys Ile
 100 105 110

att ggc cgc aca ctg gtg gtc cat gaa aaa gca gat gac ttg ggc aaa 501
 Ile Gly Arg Thr Leu Val Val His Glu Lys Ala Asp Asp Leu Gly Lys
 115 120 125

ggt gga aat gaa gaa agt aca aag aca gga aac gct gga agt cgt ttg 549
 Gly Gly Asn Glu Glu Ser Thr Lys Thr Gly Asn Ala Gly Ser Arg Leu
 130 135 140 145

gct tgt ggt gta att ggg atc gcc caa agatctcatc accatcacca 596
 Ala Cys Gly Val Ile Gly Ile Ala Gln
 150

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 <213> Homo sapiens

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 Phe Asn Pro Leu Ser Arg Lys His Gly Gly Pro Lys Asp Glu Glu Arg
 65 70 75 80
 His Val Gly Asp Leu Gly Asn Val Thr Ala Asp Lys Asp Gly Val Ala
 85 90 95
 Asp Val Ser Ile Glu Asp Ser Val Ile Ser Leu Ser Gly Asp His Cys
 100 105 110
 Ile Ile Gly Arg Thr Leu Val Val His Glu Lys Ala Asp Asp Leu Gly
 115 120 125
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 130 135 140
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 145 150

<210> 17
 <211> 5555
 <212> DNA
 <213> Homo sapiens

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 <223> histidine tagged calcineurin A alpha1

<220>
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 <222> (1717)..(1758)
 <223> ribosomal binding site, multiple cloning site 2

<220>
 <221> CDS
 <222> (1759)..(2271)
 <223> calcineurin B

<220>
 <221> variation
 <222> (115)..(1716)
 <223> splicevariant: histidine tagged calcineurin A
 alpha1 lacking pos: 208 - 2317 (phosphatase
 domain), newly generated N-terminus exhibits
 protease activity

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 aga gga tcg cat cac cat cac cat cac gga tcc atg tcc gag ccc aag 165
 Arg Gly Ser His His His His His Gly Ser Met Ser Glu Pro Lys
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 Ala Ile Asp Pro Lys Leu Ser Thr Thr Asp Arg Val Val Lys Ala Val
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 Asp Gly Lys Pro Arg Val Asp Ile Leu Lys Ala His Leu Met Lys Glu
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Ala	Ser	Ile	Leu	Arg	Gln	Glu	Lys	Asn	Leu	Leu	Asp	Ile	Asp	Ala	Pro	85	90	95	
Val	Thr	Val	Cys	Gly	Asp	Ile	His	Gly	Gln	Phe	Phe	Asp	Leu	Met	Lys	100	105	110	
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Gly	Asp	Tyr	Val	Asp	Arg	Gly	Tyr	Phe	Ser	Ile	Glu	Cys	Val	Leu	Tyr	130	135	140	
Leu	Trp	Ala	Leu	Lys	Ile	Leu	Tyr	Pro	Lys	Thr	Leu	Phe	Leu	Leu	Arg	145	150	155	160
Gly	Asn	His	Glu	Cys	Arg	His	Leu	Thr	Glu	Tyr	Phe	Thr	Phe	Lys	Gln	165	170	175	
Glu	Cys	Lys	Ile	Lys	Tyr	Ser	Glu	Arg	Val	Tyr	Asp	Ala	Cys	Met	Asp	180	185	190	
Ala	Phe	Asp	Cys	Leu	Pro	Leu	Ala	Ala	Leu	Met	Asn	Gln	Gln	Phe	Leu	195	200	205	
Cys	Val	His	Gly	Gly	Leu	Ser	Pro	Glu	Ile	Asn	Thr	Leu	Asp	Asp	Ile	210	215	220	
Arg	Lys	Leu	Asp	Arg	Phe	Lys	Glu	Pro	Pro	Ala	Tyr	Gly	Pro	Met	Cys	225	230	235	240

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 Ile Leu Arg Ala His Glu Ala Gln Asp Ala Gly Tyr Arg Met Tyr Arg
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 Pro Asn Tyr Leu Asp Val Tyr Asn Asn Lys Ala Ala Val Leu Lys Tyr
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Asp Gly Asn Gly Glu Val Asp Phe Lys Glu Phe Ile Glu Gly Val Ser
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Gln Phe Ser Val Lys Gly Asp Lys Glu Gln Lys Leu Arg Phe Ala Phe
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Arg Ile Tyr Asp Met Asp Lys Asp Gly Tyr Ile Ser Asn Gly Glu Leu
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Phe Gln Val Leu Lys Met Met Val Gly Asn Asn Leu Lys Asp Thr Gln
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Leu Gln Gln Ile Val Asp Lys Thr Ile Ile Asn Ala Asp Lys Asp Gly
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 Val Thr Val Cys Gly Asp Ile His Gly Gln Phe Phe Asp Leu Met Lys
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 Gly Asn His Glu Cys Arg His Leu Thr Glu Tyr Phe Thr Phe Lys Gln
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 Glu Cys Lys Ile Lys Tyr Ser Glu Arg Val Tyr Asp Ala Cys Met Asp
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 Ala Phe Asp Cys Leu Pro Leu Ala Ala Leu Met Asn Gln Gln Phe Leu
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 Cys Val His Gly Gly Leu Ser Pro Glu Ile Asn Thr Leu Asp Asp Ile
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 Arg Lys Leu Asp Arg Phe Lys Glu Pro Pro Ala Tyr Gly Pro Met Cys
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 Asp Ile Leu Trp Ser Asp Pro Leu Glu Asp Phe Gly Asn Glu Lys Thr
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Ala Arg Ala Ala Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Gly
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Ala Asp Arg Val Val Lys Ala Val Pro Phe Pro Pro Thr His Arg Leu
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Thr Ser Glu Glu Val Phe Asp Leu Asp Gly Ile Pro Arg Val Asp Val
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Leu Lys Asn His Leu Val Lys Glu Gly Arg Val Asp Glu Glu Ile Ala
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Leu Arg Ile Ile Asn Glu Gly Ala Ala Ile Leu Arg Arg Glu Lys Thr
85 90 95

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Met Ile Glu Val Glu Ala Pro Ile Thr Val Cys Gly Asp Ile His Gly
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 Leu Thr Ser Glu Glu Val Phe Asp Leu Asp Gly Ile Pro Arg Val Asp
 50 55 60
 Val Leu Lys Asn His Leu Val Lys Glu Gly Arg Val Asp Glu Glu Ile
 65 70 75 80
 Ala Leu Arg Ile Ile Asn Glu Gly Ala Ala Ile Leu Arg Arg Glu Lys
 85 90 95
 Thr Met Ile Glu Val Glu Ala Pro Ile Thr Val Cys Gly Asp Ile His
 100 105 110
 Gly Gln Phe Phe Asp Leu Met Lys Leu Phe Glu Val Gly Gly Ser Pro
 115 120 125
 Ala Asn Thr Arg Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg Gly Tyr
 130 135 140
 Phe Ser Ile Glu Cys Val Leu Tyr Leu Trp Val Leu Lys Ile Leu Tyr
 145 150 155 160
 Pro Ser Thr Leu Phe Leu Leu Arg Gly Asn His Glu Cys Arg His Leu
 165 170 175
 Thr Glu Tyr Phe Thr Phe Lys Gln Glu Cys Lys Ile Lys Tyr Ser Glu
 180 185 190
 Arg Val Tyr Glu Ala Cys Met Glu Ala Phe Asp Ser Leu Pro Leu Ala
 195 200 205
 Ala Leu Leu Asn Gln Gln Phe Leu Cys Val His Gly Gly Leu Ser Pro
 210 215 220
 Glu Ile His Thr Leu Asp Asp Ile Arg Arg Leu Asp Arg Phe Lys Glu

225		230		235		240
Pro Pro Ala Phe Gly	Pro Met Cys Asp	Leu Leu Trp Ser Asp	Pro Ser			
	245		250		255	
Glu Asp Phe Gly Asn	Glu Lys Ser Gln	Glu His Phe Ser His	Asn Thr			
	260		265		270	
Val Arg Gly Cys Ser Tyr	Phe Tyr Asn Tyr	Pro Ala Val Cys	Glu Phe			
	275		280		285	
Leu Gln Asn Asn Asn	Leu Leu Ser Ile	Ile Arg Ala His	Glu Ala Gln			
	290		295		300	
Asp Ala Gly Tyr Arg	Met Tyr Arg Lys	Ser Gln Thr Thr	Gly Phe Pro			
305		310		315		320
Ser Leu Ile Thr Ile	Phe Ser Ala Pro	Asn Tyr Leu Asp	Val Tyr Asn			
	325		330		335	
Asn Lys Ala Ala Val	Leu Lys Tyr Glu	Asn Asn Val Met	Asn Ile Arg			
	340		345		350	
Gln Phe Asn Cys Ser	Pro His Pro Tyr	Trp Leu Pro Asn	Phe Met Asp			
	355		360		365	
Val Phe Thr Trp Ser	Leu Pro Phe Val	Gly Glu Lys Val	Thr Glu Met			
	370		375		380	
Leu Val Asn Val Leu	Ser Ile Cys Ser Asp	Asp Glu Leu Met	Thr Glu			
385		390		395		400
Gly Glu Asp Gln Phe	Asp Gly Ser Ala	Ala Ala Arg Lys	Glu Ile Ile			
	405		410		415	
Arg Asn Lys Ile Arg	Ala Ile Gly Lys	Met Ala Arg Val	Phe Ser Val			
	420		425		430	
Leu Arg Glu Glu Ser	Glu Ser Val Leu	Thr Leu Lys Gly	Leu Thr Pro			
	435		440		445	
Thr Gly Met Leu Pro	Ser Gly Val Leu	Ala Gly Gly Arg	Gln Thr Leu			
	450		455		460	
Gln Ser Ala Thr Val	Glu Ala Ile Glu	Ala Glu Lys Ala	Ile Arg Gly			
465		470		475		480
Phe Ser Pro Pro His	Arg Ile Cys Ser	Phe Glu Glu Ala	Lys Gly Leu			
	485		490		495	
Asp Arg Ile Asn Glu	Arg Met Pro Pro	Arg Lys Asp Ala	Val Gln Gln			
	500		505		510	
Asp Gly Phe Asn Ser	Leu Asn Thr Ala	His Ala Thr Glu	Asn His Gly			
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Thr Gly Asn His Thr	Ala Gln					
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<212> PRT

<213> Homo sapiens

<400> 25

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 20 25 30

Asp Asn Ser Gly Ser Leu Ser Val Glu Glu Phe Met Ser Xaa Pro Glu
 35 40 45

Leu Gln Gln Asn Xaa Leu Val Gln Arg Val Ile Asp Ile Phe Asp Thr
 50 55 60

Asp Gly Asn Gly Glu Val Asp Phe Lys Glu Phe Ile Glu Xaa Val Ser
 65 70 75 80

Gln Phe Ser Val Lys Gly Asp Lys Glu Gln Lys Leu Arg Phe Ala Phe
 85 90 95

Arg Ile Tyr Asp Met Asp Lys Asp Gly Tyr Ile Ser Asn Gly Glu Leu
 100 105 110

Phe Gln Xaa Xaa Lys Met Met Val Gly Asn Asn Leu Lys Asp Thr Gln
 115 120 125

Leu Gln Gln Ile Val Asp Lys Thr Ile Ile Asn Ala Asp Lys Asp Xaa
 130 135 140

Asp Gly Arg Ile Ser Phe Glu Glu Phe Cys Ala Val Val Xaa Gly Leu
 145 150 155 160

Asp Ile His Lys Lys Met Val Val Asp Val
 165 170

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<211> 5611

<212> DNA

<213> Homo sapiens

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<222> (115)..(1776)

<223> histidine tagged calcineurin A beta2

<220>

<221> misc feature

<222> (1777)..(1814)

<223> ribosomal binding site, multiple cloning site 2

<220>

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<222> (1815)..(2327)

<223> calcineurin B

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Met
1

aga gga tcg cat cac cat cac cat cac gga tcc gcc gcc ccg gag ccg 165
Arg Gly Ser His His His His His His Gly Ser Ala Ala Pro Glu Pro
5 10 15

gcc cgg gct gca ccg ccc cca ccc ccg ccc ccg ccg ccc cct ccc ggg 213
Ala Arg Ala Ala Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Gly
20 25 30

gct gac cgc gtc gtc aaa gct gtc cct ttc ccc cca aca cat cgc ttg 261
Ala Asp Arg Val Val Lys Ala Val Pro Phe Pro Pro Thr His Arg Leu
35 40 45

aca tct gaa gaa gta ttt gat ttg gat ggg ata ccc agg gtt gat gtt 309
Thr Ser Glu Glu Val Phe Asp Leu Asp Gly Ile Pro Arg Val Asp Val
50 55 60 65

ctg aag aac cac ttg gtg aaa gaa ggt cga gta gat gaa gaa att gcg 357
Leu Lys Asn His Leu Val Lys Glu Gly Arg Val Asp Glu Glu Ile Ala
70 75 80

ctt aga att atc aat gag ggt gct gcc atc ctt cgg aga gag aaa acc 405
Leu Arg Ile Ile Asn Glu Gly Ala Ala Ile Leu Arg Arg Glu Lys Thr
85 90 95

atg ata gaa gta gaa gct cca atc aca gtg tgt ggt gac atc cat ggc 453
Met Ile Glu Val Glu Ala Pro Ile Thr Val Cys Gly Asp Ile His Gly
100 105 110

caa ttt ttt gat ctg atg aaa ctt ttt gaa gta gga gga tca cct gct 501
Gln Phe Phe Asp Leu Met Lys Leu Phe Glu Val Gly Gly Ser Pro Ala
115 120 125

aat aca cga tac ctt ttt ctt ggc gat tat gtg gac aga ggt tat ttt 549
Asn Thr Arg Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg Gly Tyr Phe
130 135 140 145

agt ata gag cat gtt cta ggc act gaa gac ata tcg att aat cct cac 597
Ser Ile Glu His Val Leu Gly Thr Glu Asp Ile Ser Ile Asn Pro His
150 155 160

aat aat att aat gag tgt gtc tta tat tta tgg gtt ctg aag att cta 645
Asn Asn Ile Asn Glu Cys Val Leu Tyr Leu Trp Val Leu Lys Ile Leu
165 170 175

tac cca agc aca tta ttt ctt ctg aga ggc aac cat gaa tgc aga cac 693
Tyr Pro Ser Thr Leu Phe Leu Leu Arg Gly Asn His Glu Cys Arg His
180 185 190

ctt act gaa tat ttt acc ttt aag cag gaa tgt aaa att aag tat tcg 741
Leu Thr Glu Tyr Phe Thr Phe Lys Gln Glu Cys Lys Ile Lys Tyr Ser
195 200 205

gaa aga gtc tat gaa gct tgt atg gaa gct ttt gat agt ttg cct ctt 789
Glu Arg Val Tyr Glu Ala Cys Met Glu Ala Phe Asp Ser Leu Pro Leu
210 215 220 225

gct gca ctt tta aac caa cag ttt ctt tgt gtt cat ggt gga ctt tca 837
Ala Ala Leu Leu Asn Gln Gln Phe Leu Cys Val His Gly Gly Leu Ser

230	235	240	
cca gaa ata cac aca ctg gat gat att agg aga tta gat aga ttc aaa Pro Glu Ile His Thr Leu Asp Asp Ile Arg Arg Leu Asp Arg Phe Lys 245 250 255			885
gag cca cct gca ttt gga cca atg tgt gac ttg tta tgg tcc gat cct Glu Pro Pro Ala Phe Gly Pro Met Cys Asp Leu Leu Trp Ser Asp Pro 260 265 270			933
tct gaa gat ttt gga aat gaa aaa tca cag gaa cat ttt agt cac aat Ser Glu Asp Phe Gly Asn Glu Lys Ser Gln Glu His Phe Ser His Asn 275 280 285			981
aca gtt cga gga tgt tct tat ttt tat aac tat cca gca gtg tgt gaa Thr Val Arg Gly Cys Ser Tyr Phe Tyr Asn Tyr Pro Ala Val Cys Glu 290 295 300 305			1029
ttt ttg caa aac aat aat ttg tta tcg att att aga gct cat gaa gct Phe Leu Gln Asn Asn Asn Leu Leu Ser Ile Ile Arg Ala His Glu Ala 310 315 320			1077
caa gat gca ggc tat aga atg tac aga aaa agt caa act aca ggg ttc Gln Asp Ala Gly Tyr Arg Met Tyr Arg Lys Ser Gln Thr Thr Gly Phe 325 330 335			1125
cct tca tta ata aca att ttt tcg gca cct aat tac tta gat gtc tac Pro Ser Leu Ile Thr Ile Phe Ser Ala Pro Asn Tyr Leu Asp Val Tyr 340 345 350			1173
aat aat aaa gct gct gta tta aag tat gaa aat aat gtg atg aat att Asn Asn Lys Ala Ala Val Leu Lys Tyr Glu Asn Asn Val Met Asn Ile 355 360 365			1221
cga cag ttt aac tgt tct cca cat cct tac tgg ttg cct aat ttt atg Arg Gln Phe Asn Cys Ser Pro His Pro Tyr Trp Leu Pro Asn Phe Met 370 375 380 385			1269
gat gtc ttc acg tgg tct tta ccg ttt gtt gga gaa aaa gtg aca gaa Asp Val Phe Thr Trp Ser Leu Pro Phe Val Gly Glu Lys Val Thr Glu 390 395 400			1317
atg ttg gta aat gtt ctg agt att tgc tct gat gat gaa cta atg act Met Leu Val Asn Val Leu Ser Ile Cys Ser Asp Asp Glu Leu Met Thr 405 410 415			1365
gaa ggt gaa gac cag ttt gat ggt tca gct gca gcc cgg aaa gaa atc Glu Gly Glu Asp Gln Phe Asp Gly Ser Ala Ala Ala Arg Lys Glu Ile 420 425 430			1413
ata aga aac aaa att cga gca att ggc aag atg gca aga gtc ttc tct Ile Arg Asn Lys Ile Arg Ala Ile Gly Lys Met Ala Arg Val Phe Ser 435 440 445			1461
gtt ctc agg gag gag agt gaa agt gtg ctg aca ctc aag ggc ctg act Val Leu Arg Glu Glu Ser Glu Ser Val Leu Thr Leu Lys Gly Leu Thr 450 455 460 465			1509
ccc aca ggg atg ttg cct agt gga gtg tta gct gga gga cgg cag acc Pro Thr Gly Met Leu Pro Ser Gly Val Leu Ala Gly Gly Arg Gln Thr 470 475 480			1557

ctg caa agt gcc aca gtt gag gct att gag gct gaa aaa gca ata cga 1605
 Leu Gln Ser Ala Thr Val Glu Ala Ile Glu Ala Glu Lys Ala Ile Arg
 485 490 495

gga ttc tct cca cca cat aga atc tgc agt ttt gaa gag gca aag ggt 1653
 Gly Phe Ser Pro Pro His Arg Ile Cys Ser Phe Glu Glu Ala Lys Gly
 500 505 510

ttg gat agg atc aat gag aga atg cca cct cgg aaa gat gct gta cag 1701
 Leu Asp Arg Ile Asn Glu Arg Met Pro Pro Arg Lys Asp Ala Val Gln
 515 520 525

caa gat ggt ttc aat tct ctg aac acc gca cat gcc act gag aac cac 1749
 Gln Asp Gly Phe Asn Ser Leu Asn Thr Ala His Ala Thr Glu Asn His
 530 535 540 545

ggg acg ggc aac cat act gcc cag tga ttaactaggg taccgccggg 1796
 Gly Thr Gly Asn His Thr Ala Gln
 550

aaagaggaga aattaact atg gga aat gag gca agt tat cct ttg gaa atg 1847
 Met Gly Asn Glu Ala Ser Tyr Pro Leu Glu Met
 555 560 565

tgc tca cac ttt gat gcr gat gaa att aaa agg cta gga aag aga ttt 1895
 Cys Ser His Phe Asp Xaa Asp Glu Ile Lys Arg Leu Gly Lys Arg Phe
 570 575 580

aag aag cty gat ttg gac aat tct ggt tct ttg agt gtg gaa gag ttc 1943
 Lys Lys Xaa Asp Leu Asp Asn Ser Gly Ser Leu Ser Val Glu Glu Phe
 585 590 595

atg tct ctr cct gag tta caa cag aat ccy tta gta cag cga gta ata 1991
 Met Ser Xaa Pro Glu Leu Gln Asn Xaa Leu Val Gln Arg Val Ile
 600 605 610

gat ata ttc gac aca gat ggg aat gga gaa gta gac ttt aaa gar ttc 2039
 Asp Ile Phe Asp Thr Asp Gly Asn Gly Glu Val Asp Phe Lys Glu Phe
 615 620 625

att gag ggm gtc tct cag ttc agt gtc aaa gga gat aag gar cag aar 2087
 Ile Glu Xaa Val Ser Gln Phe Ser Val Lys Gly Asp Lys Glu Gln Lys
 630 635 640 645

ttg agg ttt gct ttc cgt atc tat gac atg gat aaa gay ggc tat att 2135
 Leu Arg Phe Ala Phe Arg Ile Tyr Asp Met Asp Lys Asp Gly Tyr Ile
 650 655 660

tcc aat ggg gaa ctc ttc cag gtr ytr aag atg atg gtg ggg aac aat 2183
 Ser Asn Gly Glu Leu Phe Gln Xaa Xaa Lys Met Met Val Gly Asn Asn
 665 670 675

ctg aaa gat aca cag tta cag caa att gta gac aaa acc ata ata aat 2231
 Leu Lys Asp Thr Gln Leu Gln Ile Val Asp Lys Thr Ile Ile Asn
 680 685 690

gca gat aag gat ggr gat gga aga ata tcc ttt gaa gaa ttc tgt gct 2279
 Ala Asp Lys Asp Xaa Asp Gly Arg Ile Ser Phe Glu Glu Phe Cys Ala
 695 700 705

gtt gta ggy ggc cta gat atc cac aaa aag atg gtg gta gat gtg tga 2327
 Val Val Xaa Gly Leu Asp Ile His Lys Lys Met Val Val Asp Val

710 715 720 725

ttaattagaa gcttaattag ctgagcttgg actcctggtg atagatccag taatgacctc 2387
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<211> 553

<212> PRT

<213> Homo sapiens

<400> 27

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Pro Ala Arg Ala Ala Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro
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Gly Ala Asp Arg Val Val Lys Ala Val Pro Phe Pro Pro Thr His Arg
 35 40 45
 Leu Thr Ser Glu Glu Val Phe Asp Leu Asp Gly Ile Pro Arg Val Asp
 50 55 60
 Val Leu Lys Asn His Leu Val Lys Glu Gly Arg Val Asp Glu Glu Ile
 65 70 75 80
 Ala Leu Arg Ile Ile Asn Glu Gly Ala Ala Ile Leu Arg Arg Glu Lys
 85 90 95
 Thr Met Ile Glu Val Glu Ala Pro Ile Thr Val Cys Gly Asp Ile His
 100 105 110
 Gly Gln Phe Phe Asp Leu Met Lys Leu Phe Glu Val Gly Gly Ser Pro
 115 120 125
 Ala Asn Thr Arg Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg Gly Tyr
 130 135 140
 Phe Ser Ile Glu His Val Leu Gly Thr Glu Asp Ile Ser Ile Asn Pro
 145 150 155 160
 His Asn Asn Ile Asn Glu Cys Val Leu Tyr Leu Trp Val Leu Lys Ile
 165 170 175
 Leu Tyr Pro Ser Thr Leu Phe Leu Leu Arg Gly Asn His Glu Cys Arg
 180 185 190
 His Leu Thr Glu Tyr Phe Thr Phe Lys Gln Glu Cys Lys Ile Lys Tyr
 195 200 205
 Ser Glu Arg Val Tyr Glu Ala Cys Met Glu Ala Phe Asp Ser Leu Pro
 210 215 220
 Leu Ala Ala Leu Leu Asn Gln Gln Phe Leu Cys Val His Gly Gly Leu
 225 230 235 240
 Ser Pro Glu Ile His Thr Leu Asp Asp Ile Arg Arg Leu Asp Arg Phe
 245 250 255
 Lys Glu Pro Pro Ala Phe Gly Pro Met Cys Asp Leu Leu Trp Ser Asp
 260 265 270
 Pro Ser Glu Asp Phe Gly Asn Glu Lys Ser Gln Glu His Phe Ser His
 275 280 285
 Asn Thr Val Arg Gly Cys Ser Tyr Phe Tyr Asn Tyr Pro Ala Val Cys
 290 295 300
 Glu Phe Leu Gln Asn Asn Asn Leu Leu Ser Ile Ile Arg Ala His Glu
 305 310 315 320
 Ala Gln Asp Ala Gly Tyr Arg Met Tyr Arg Lys Ser Gln Thr Thr Gly
 325 330 335
 Phe Pro Ser Leu Ile Thr Ile Phe Ser Ala Pro Asn Tyr Leu Asp Val
 340 345 350
 Tyr Asn Asn Lys Ala Ala Val Leu Lys Tyr Glu Asn Asn Val Met Asn

-67-

355 360 365
 Ile Arg Gln Phe Asn Cys Ser Pro His Pro Tyr Trp Leu Pro Asn Phe
 370 375 380
 Met Asp Val Phe Thr Trp Ser Leu Pro Phe Val Gly Glu Lys Val Thr
 385 390 395 400
 Glu Met Leu Val Asn Val Leu Ser Ile Cys Ser Asp Asp Glu Leu Met
 405 410 415
 Thr Glu Gly Glu Asp Gln Phe Asp Gly Ser Ala Ala Ala Arg Lys Glu
 420 425 430
 Ile Ile Arg Asn Lys Ile Arg Ala Ile Gly Lys Met Ala Arg Val Phe
 435 440 445
 Ser Val Leu Arg Glu Glu Ser Glu Ser Val Leu Thr Leu Lys Gly Leu
 450 455 460
 Thr Pro Thr Gly Met Leu Pro Ser Gly Val Leu Ala Gly Gly Arg Gln
 465 470 475 480
 Thr Leu Gln Ser Ala Thr Val Glu Ala Ile Glu Ala Glu Lys Ala Ile
 485 490 495
 Arg Gly Phe Ser Pro Pro His Arg Ile Cys Ser Phe Glu Glu Ala Lys
 500 505 510
 Gly Leu Asp Arg Ile Asn Glu Arg Met Pro Pro Arg Lys Asp Ala Val
 515 520 525
 Gln Gln Asp Gly Phe Asn Ser Leu Asn Thr Ala His Ala Thr Glu Asn
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 His Gly Thr Gly Asn His Thr Ala Gln
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<210> 28

<211> 170

<212> PRT

<213> Homo sapiens

<400> 28

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 20 25 30
 Asp Asn Ser Gly Ser Leu Ser Val Glu Glu Phe Met Ser Xaa Pro Glu
 35 40 45
 Leu Gln Gln Asn Xaa Leu Val Gln Arg Val Ile Asp Ile Phe Asp Thr
 50 55 60
 Asp Gly Asn Gly Glu Val Asp Phe Lys Glu Phe Ile Glu Xaa Val Ser
 65 70 75 80
 Gln Phe Ser Val Lys Gly Asp Lys Glu Gln Lys Leu Arg Phe Ala Phe
 85 90 95

Arg Ile Tyr Asp Met Asp Lys Asp Gly Tyr Ile Ser Asn Gly Glu Leu
 100 105 110

Phe Gln Xaa Xaa Lys Met Met Val Gly Asn Asn Leu Lys Asp Thr Gln
 115 120 125

Leu Gln Gln Ile Val Asp Lys Thr Ile Ile Asn Ala Asp Lys Asp Xaa
 130 135 140

Asp Gly Arg Ile Ser Phe Glu Glu Phe Cys Ala Val Val Xaa Gly Leu
 145 150 155 160

Asp Ile His Lys Lys Met Val Val Asp Val
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<210> 29
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 <223> ribosomal binding site, multiple cloning site 2

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 Met
 1

aga gga tcg cat cac cat cac cat cac gga tcc atg tcc ggg agg cgc 165
 Arg Gly Ser His His His His His Gly Ser Met Ser Gly Arg Arg
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ttc cac ctc tcc acc acc gac cgc gtc atc aaa gct gtc ccc ttt cct 213
 Phe His Leu Ser Thr Thr Asp Arg Val Ile Lys Ala Val Pro Phe Pro
 20 25 30

cca acc caa cgg ctt act ttc aag gaa gta ttt gag aat ggg aaa cct 261
 Pro Thr Gln Arg Leu Thr Phe Lys Glu Val Phe Glu Asn Gly Lys Pro
 35 40 45

aaa gtt gat gtt tta aaa aac cat ttg gta aag gaa gga cga ctg gaa 309
 Lys Val Asp Val Leu Lys Asn His Leu Val Lys Glu Gly Arg Leu Glu
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SUBSTITUTE SHEET (RULE 26)

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 Thr Glu Met Leu Val Asn Val Leu Asn Ile Cys Ser Asp Asp Glu Leu
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ccc aca ggc aca ctc cct ctg ggc gtc ctc tca gga ggc aag cag act 1461
 Pro Thr Gly Thr Leu Pro Leu Gly Val Leu Ser Gly Gly Lys Gln Thr
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aat gag gca agt tat cct ttg gaa atg tgc tca cac ttt gat gca gat 1755
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 His Lys Lys Met Val Val Asp Val
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Gly	Asp	Ile	His	Gly	Gln	Phe	Phe	Asp	Leu	Met	Lys	Leu	Phe	Glu	Val	100	105	110	
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Asp	Arg	Gly	Tyr	Phe	Ser	Ile	Glu	Cys	Val	Leu	Tyr	Leu	Trp	Ser	Leu	130	135	140	
Lys	Ile	Asn	His	Pro	Lys	Thr	Leu	Phe	Leu	Leu	Arg	Gly	Asn	His	Glu	145	150	155	160
Cys	Arg	His	Leu	Thr	Asp	Tyr	Phe	Thr	Phe	Lys	Gln	Glu	Cys	Arg	Ile	165	170	175	
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-75-

His Ser

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 cytoskeleton, death-domain homolog, stomatin
 homolog

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Pro Thr Gln Arg Leu Thr Phe Lys Glu Val Phe Glu Asn Gly Lys Pro
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Lys Val Asp Val Leu Lys Asn His Leu Val Lys Glu Gly Arg Leu Glu
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Arg His Leu Thr Asp Tyr Phe Thr Phe Lys Gln Glu Cys Arg Ile Lys
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 His Arg Ser Asp Gln Gly Lys Lys Ala His Ser
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Pro Lys Val Asp Val Leu Lys Asn His Leu Val Lys Glu Gly Arg Leu
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Glu Glu Glu Val Ala Leu Lys Ile Ile Asn Asp Gly Ala Ala Ile Leu
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Arg Gln Glu Lys Thr Met Ile Glu Val Asp Ala Pro Ile Thr Val Cys
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Thr Gly Phe Pro Ser Leu Ile Thr Ile Phe Ser Ala Pro Asn Tyr Leu

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